



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/677,877

Source:

IFWO-

Date Processed by STIC:

4/9/84

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
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Revised 10/08/03



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/677,877

DATE: 04/09/2004

TIME: 15:37:16

Input Set : A:\PTO.LN.txt

Output Set: N:\CRF4\04092004\J677877.raw

SEQUENCE LISTING

Insert these Mandatory headings With Response:

(I) Applicant:

(II) Title of Invention:

(iii) NUMBER OF SEQUENCES: 16 (insert)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US/10/677,877

(B) FILING DATE: 02-Oct-2003

(v) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE:

(B) STREET:

(C) CITY:

(D) STATE:

(E) COUNTRY:

(F) ZIP:

(M) COMPUTER READABLE FORM:

(A) MEDIUM TYPE:

(B) COMPUTER:

(C) OPERATING SYSTEM:

(D) SOFTWARE:

(N) CURRENT ATTUATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

ERRORED SEQUENCES

6 (2) INFORMATION FOR SEQ ID NO: 1:

7 (i) SEQUENCE CHARACTERISTICS:

8 (A) LENGTH: 963 base pairs

9 (B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

11 (D) TOPOLOGY: linear

12 (ii) MOLECULE TYPE: cDNA

W--> 13 (iii) HYPOTHETICAL: N

W--> 14 (iv) ANTI-SENSE: N

15 (vi) ORIGINAL SOURCE:

16 (A) ORGANISM: Homo sapiens

18 (vii) IMMEDIATE SOURCE:

19 (B) CLONE: pTrimer(T0)

20 (ix) FEATURE:

21 (A) NAME/KEY: CDS

22 (B) LOCATION: 12..947

23 (D) OTHER INFORMATION:

24 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

delete

E--> 27 Hind III BglII

E--> 28 AAGCTTACGTAAGATCTAACGGTCTCCCTGGCCCCATTGGGCCCCCTGGTCCCTCG 55

E--> 29 CGGTCCGCACTGGTGTGCTGGTCTGTTGGTCCCCCGGCCCTCTGGACCTCCT 110

E--> 30 GGTCCCCCTGGTCTCCAGCGCTGGTTTCGACTTCAGCTTCTTGCCCCAGCCAC 165

E--> 31 CTCGAAGAAGGCTCAGCATGGTGGCCGCTACTACCGGGCTGATGATGCCAATGT 220

E--> 32 GGTTCGTGACCGTGACCTCGAGGTGGACACCACCTCAAGAGCCTGAGCCAGCAG

E--> 33 ATCGAGAACATCCGGAGCCAGAGGGAAGCCGAAGAACCCCGCCCGACCTGCC

E--> 34 GTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCC

E--> 35 CAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGT

E--> 36 GAGACCTGCGTGTACCCCACTCAGCCAGTGTGGCCCAAGAAGTGGTACATCA

E--> 37 GCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCCGGCGAGAGCATGACCGATGG

E--> 38 ATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATGTGGCCATCCAG

E--> 39 CTGACCTTCTGCGCCTGATGTCCACCGAGGCCTCCCAAGACATCACCTACCACT

E--> 40 GCAAGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGCCCT

E--> 41 GCTCCTCAAGGGCTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTC

Does Not Comply
Corrected Diskette Needed

(Pg. 1-15)

Suggestion: Consult
Sequence Rules for
Valid format.

please insert
numbers at the
end of sequence.

please
group in
10 bases
each
Nucleotide

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PATENT APPLICATION: US/10/677,877

DATE: 04/09/2004

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Input Set : A:\PTO.LN.txt

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E--> 42 ACCTACAGCGTCACTGTGCGATGGCTGCACGAGTCACACCGGAGCCTGGGGCAAGA
 E--> 43 CAGTGATTGAATACAAAACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGC
 E--> 44 CCCCTTGGACGTTGGTGGCCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTC
 E--> 45 TGCTTCCTGTAAACTCCCTCCATCTAGA
 E--> 46 ~~Xba I delete~~

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 311 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

1 RSNGLPGPIG PPGPRGRTGD AGFVGPPGPP GPPGPPGPPS AGFDFSFLPQ PPQEKADGG 60
 61 RYRADDANV VRDRDLEVDL TLKSLSQIE NIRSPEGSRK NPARTCRDLK MCHSDWKSGE 120
 121 YWIDPNQGCN LDAIKVFCNM ETGETCVYPT QPSVAQKNWY ISKNPKDKRH VWFGESMTDG 180
 181 FQFEYGGQGS DPADVAILTL FLRLMSTEAS QNITYHCKNS VAYMDQQTGN LKKALLLKGS 240
 241 NEIEIRAEGN SRFTYSVTVD GCTSHTGAWG KTVIEYKTTK SSRLPIIDVA PLDVGAPDQE 300

E--> 64 ~~301 FGFDVGPVCF L~~

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 771 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(B) CLONE: pTrimer(T2)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 12..755

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3

E--> 88 ~~Hind III BglII delete~~
 E--> 89 AAGCTTACGTAAGATCTGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCACCT
 E--> 90 CAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGAAGCCGCAAGAACCCCGCC
 E--> 91 CGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACC
 E--> 92 CCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTG
 E--> 93 CGTGTACCCCACTCAGCCCACTGTGGCCAGAGAAGTGGTACATCAGCAAGAACCCCAAGGAC
 E--> 94 AAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGG
 E--> 95 GCTCCGACCCTGCCGATGTGGCCATCCAGCTGACCTTCCTGCGCCTGATGTCCACCGAGGCCTC
 E--> 96 CCAGAACATCACCTACCACTGCAAGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAACCTC
 E--> 97 AAGAAGGCCCTGCTCCTCAAGGGCTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCT
 E--> 98 TCACCTACAGCGTCACTGTGCGATGGCTGCACGAGTCACACCGGAGCCTGGGGCAAGACAGTGAT

Insert to total at end, same error
 please group nucleotides in base pairs
 10
 invalid amino acid designators.
 Use three-letter amino acids and number them under every 5 amino acids.
 delete nos.

Do not use TAB codes between amino acid numbers. Use space characters, instead. TAB codes cause error.

Insert, same error
 please group nucleotides in 10 base pairs

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Output Set: N:\CRF4\04092004\J677877.raw

E--> 99 TGAATACAAAACCAAGTCCCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGT
 E--> 100 GCCCCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTGTAAACTCCCTCCATCT
 E--> 101 AGA
 E--> 102 ~~Xba I~~ delete
 105 (2) INFORMATION FOR SEQ ID NO: 4:
 106 (i) SEQUENCE CHARACTERISTICS:
 107 (A) LENGTH: 247 amino acids
 108 (B) TYPE: amino acid
 109 (D) TOPOLOGY: linear
 110 (ii) MOLECULE TYPE: protein
 111 (vi) ORIGINAL SOURCE:
 112 (A) ORGANISM: Homo sapiens
 113 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4
 116 1 RSDANVVRDR DLEVDTTLS LSQQIENIRS PEGSRKNPAR TCRDLKMCHS DWKSGEYWID 60
 117 61 PNQGCNLDAI KVFCNMETGE TCVYPTQPSV AQKNWYISKV PKDKRHVWFG ESMTDGFQFE 120
 118 121 YGGQGSDDPAD VAIQLTFLRL MSTEASQNT YHCKNSVAYM DQQTGNLKA LLLKGSNEIE 180
 119 181 IRAEGNSRFT YSVTVDGCTS HTGAWGKTVI EYKTTKSSRL PIIDVAPLDV GAPDQEFQFD 240
 E--> 120 ~~247~~ VGPVCFLL
 123 (2) INFORMATION FOR SEQ ID NO: 5:
 124 (i) SEQUENCE CHARACTERISTICS:
 125 (A) LENGTH: 2487 base pairs
 126 (B) TYPE: nucleic acid
 127 (C) STRANDEDNESS: double
 128 (D) TOPOLOGY: linear
 129 (ii) MOLECULE TYPE: cDNA
 W--> 130 (iii) HYPOTHETICAL: N
 W--> 131 (iv) ANTI-SENSE: N
 132 (vi) ORIGINAL SOURCE:
 133 (A) ORGANISM: Homo sapiens
 135 (vii) IMMEDIATE SOURCE:
 136 (B) CLONE: pTrimer/AP-T0
 137 (ix) FEATURE:
 138 (A) NAME/KEY: CDS
 139 (B) LOCATION: 12..2471
 140 (D) OTHER INFORMATION:
 141 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5
 E--> 144 ~~Hind III~~ delete
 E--> 145 AAGCTTCCTGCATGCTGCTGCTGCTGCTGCTGCTGGGCTGAGGCTACAGCTCTCCCTG 59
 E--> 146 GGCATCATCCCAGTTGAGGAGGAGAACCCGGACTTCTGGAACCGCGAGGCAGCCGAGGC 118
 E--> 147 CCTGGGTGCCGCCAAGAAGCTGCAGCCTGCACAGACAGCCGCCAAGAACCTCATCATCT 236
 E--> 148 TCCTGGGCGATGGGATGGGGGTGTCTACGGTGACAGCTGCCAGGATCCTAAAAGGGCAG
 E--> 149 AAGAAGGACAACTGGGGCTGAGATACCCCTGGCCATGGACCGCTTCCCATATGTGGC
 E--> 150 TCTGTCCAAGACATACAATGTAGACAAACATGTGCCAGACAGTGGAGCCACAGCCACGG
 E--> 151 CCTACCTGTGCGGGGTCAAGGGCAACTTCCAGACCATTGGCTTGAGTGCAGCCGCCCGC
 E--> 152 TTTAACCAGTGCAACACGACACGCGGCAACGAGGTCTCCGTGATGAATCGGGCCAA
 E--> 153 GAAAGCAGGGAAGTCAGTGGGAGTGGTAACCAACACACGAGTGCAGCACGCCCTCGCCAG
 E--> 154 CCGGCACCTACGCCACACGGTGAACCGCAACTGGTACTCGGACGCCGACGTGCCTGCC
 E--> 155 TCGGCCCGCCAGGAGGGGTGCCAGGACATCGCTACGCAGCTCATCTCCAACATGGACAT
 E--> 156 TGACGTGATCCTAGGTGGAGGCCGAAAGTACATGTTTCCCATGGGAACCCAGACCCTG

Insert totals
at end.

same error

same error
as sequence 2

delete

Insert
totals
same error

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E--> 157 AGTACCCAGATGACTACAGCCAAGGTGGGACCAGGCTGGACGGGAAGAATCTGGTGCAG
 E--> 158 GAATGGCTGGCGAAGCGCCAGGGTGCCCGGTATGTGTGGAACCGCACTGAGCTCATGCA
 E--> 159 GGCTTCCCTGGACCCGCTCTGTGACCCATCTCATGGGTCTCTTTGAGCCTGGAGACATGA
 E--> 160 AATACGAGATCCACCGAGACTCCACACTGGACCCCTCCCTGATGGAGATGACAGAGGCT
 E--> 161 GCCCTGCGCCTGCTGAGCAGGAACCCCGCGGCTTCTTCCTCTTCGTGGAGGGTGGTCG
 E--> 162 CATCGACCATGGTCATCATGAAAGCAGGGCTTACCGGGCACTGACTGAGACGATCATGT
 E--> 163 TCGACGACGCCATTGAGAGGGCGGGCCAGCTCACCAGCGAGGAGGACACGCTGAGCCTC
 E--> 164 GTCACCTGCCGACCACTCCCACGTCTTCTCCTTCGGAGGCTACCCCTGCGAGGGAGCTC
 E--> 165 CATCTTCGGGCTGGCCCTTGGCAAGGCCCGGACAGGAAGGCCTACACGGTCTCTCTAT
 E--> 166 ACGGAAACGGTCAAGGCTATGTGCTCAAGGACGGCGCCCGGGATGTTACCGAGAGC
 E--> 167 GAGAGCGGGAGCCCGAGTATCGGCAGCAGTCAGCAGTGCCCTGGACGAAGAGACCCA
 E--> 168 CGCAGGCGAGGACGTGGCGGTGTTTCGCGCGCGGCCCGCAGGCGCACCTGGTTCACGGCG
 E--> 169 TGCAGGAGCAGACCTTCATAGCGCACGTATGGCCTTCGCGCCTGCCTGGAGCCCTAC
 E--> 170 ACCGCCTGCGACCTGGCGCCCCCGCGGCCACCACGACGCGCGCACCCGGGTTCGGG
 E--> 171 AAGATCTAACGGTCTCCCTGGCCCCATTGGGCCCCCTGGTCTTCGCGGTGCGACTGGTG
 E--> 172 ATGCTGGTCCTGTTGGTCCCCCGGCCCTCCTGGACCTCCTGGTCCCCCTGGTCTCCC
 E--> 173 AGCGCTGGTTTTGACTTCAGCTTCCTGCCCCAGCCACCTCAAGAGAAGGCTCACGATGG
 E--> 174 TGGCCGCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGG
 E--> 175 ACACCACCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGAAGC
 E--> 176 CGCAAGAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAG
 E--> 177 TGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCT
 E--> 178 GCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCAGTGTGGCCAGAAAG
 E--> 179 AACTGGTACATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCAT
 E--> 180 GACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATGTGGCCA
 E--> 181 TCCAGCTGACCTTCCTGCGCCTGATGTCCACCGAGGCCTCCAGAACATCACCTACCAC
 E--> 182 TGCAAGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGCCCTGCT
 E--> 183 CCTCAAGGGCTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTCACCTACA
 E--> 184 GCGTCACTGTGATGGCTGCACGAGTCACACCGAGCCTGGGGCAAGACAGTGATTGAA
 E--> 185 TACAAAACCACCAAGTCTTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGG
 E--> 186 TGCCCCAGACCAGGAATTGGGCTTCGACGTTGGCCCTGTCTGCTTCTGTAACTCCCT
 E--> 187 CCATCTAGA
 E--> 188 ~~XBa I delete~~

Insert
 totals at
 end.

- same
 errors

191 (2) INFORMATION FOR SEQ ID NO: 6:

192 (i) SEQUENCE CHARACTERISTICS:

193 (A) LENGTH: 819 amino acids

194 (B) TYPE: amino acid

195 (D) TOPOLOGY: linear

196 (ii) MOLECULE TYPE: protein

197 (vi) ORIGINAL SOURCE:

198 (A) ORGANISM: Homo sapiens

199 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6

202	1	MLLLLLLLGL	RLQSLGIIP	VEENPDFWN	REAAEALGAA	KKLQPAQTAA	KNLIIFLGDG	60
203	61	MGVSTVTAAR	ILKGQKKDKL	GPEIPLAMDR	FPYVALSKTY	NVDKHPDSG	ATATAYLCGV	120
204	121	KGNFQYIGLS	AAARFNQCNT	TRGNEVISVM	NRKKAGKSV	GVVTTTRVQH	ASPAGTYAHT	180
205	181	VNRNWTSDAD	VPASARQEGC	QDIATQLISN	MDIDVILGGG	RKYMFPMGTP	DPEYPDDYSQ	240
206	241	GGTRLDGKNL	VQEWLAKRQG	ARYVWNRTSL	MQASLDPSVT	HLMGLFEPGD	MKYEIHRDST	300
207	301	LDPSLMEMTE	AALRLLSRNP	RGFFLFVEGG	RIDHGHHSR	AYRALTETIM	FDDAIERAGQ	360
208	361	LTSEEDTSL	VTADHSHVFS	FGGYPLRGSS	IFGLAPGKAR	DRKAYTVLLY	GNGPGYVLKD	420
209	421	GARPDVTESE	SGSPEYRQQS	AVPLDEETHA	GEDVAVFARG	PQAHLVHGVQ	EQTFLIAHVA	480

same
 errors

delete
 #s

RAW SEQUENCE LISTING

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PATENT APPLICATION: US/10/677,877

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Input Set : A:\PTO.LN.txt

Output Set: N:\CRF4\04092004\J677877.raw

delete #5

210	481	FAACLEPYTA CDLAPPAGTT DAAHPGSGRS NGLPGPIGPP GPRGRTGDAG PVGPPGPPGP	540
211	541	PGPPGPPSAG FDFSFLPQPP QEKAHDGGRY YRADDANVVR DRDLEVDTTL KSLSQQIENI	600
212	601	RSPEGSRKNP ARTCRDLKMC HSDWKSGEYW IDPNQGCNLD AIKVFCNMET GETCVYPTQP	660
213	661	SVAQKNWYIS KNPDKRHHVW FGESMTDGFQ FEYGGQSDP ADVAIQLTFL RLMSTEASQN	720
214	721	ITYHCKNSVA YMDQQTGNLK KALLKGSNE IEIRAEGNSR FTYSVTVDGC TSHTGAWGKT	780

E--> 215 **781** VIEYKTTKSS RLPIIDVAPL DVGAPDQEFQ FDVGPPVCF

218 (2) INFORMATION FOR SEQ ID NO: 7:

219 (i) SEQUENCE CHARACTERISTICS:

220 (A) LENGTH: 2294 base pairs

221 (B) TYPE: nucleic acid

222 (C) STRANDEDNESS: double

223 (D) TOPOLOGY: linear

224 (ii) MOLECULE TYPE: cDNA

W--> 225 (iii) HYPOTHETICAL: N

W--> 226 (iv) ANTI-SENSE: N

227 (vi) ORIGINAL SOURCE:

228 (A) ORGANISM: Homo sapiens

230 (vii) IMMEDIATE SOURCE:

231 (B) CLONE: pTrimer/AP-T2

232 (ix) FEATURE:

233 (A) NAME/KEY: CDS

234 (B) LOCATION: 12..2278

235 (D) OTHER INFORMATION:

236 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7

E--> 238 ~~Hind III~~ *delete*

E--> 239 AAGCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGGGCCGTAGGCTACAGCTCTCCCTG

E--> 240 GGCATCATCCAGTGTGAGGAGGAGAACCCGGACTTCTGGAACCGCGAGGCAGCCGAGGC

E--> 241 CCTGGGTGCCGCCAAGAAGCTGCAGCCTGCACAGACAGCCGCCAAGAACCCTCATCATCT

E--> 242 TCCTGGGCGATGGGATGGGGGTGTCTACGGTGACAGCTGCCAGGATCCTAAAAGGGCAG

E--> 243 AAGAAGGACAAACTGGGGCCTGAGATACCCCTGGCCATGGACCGCTTCCCATATGTGGC

E--> 244 TCTGTCCAAGACATACAATGTAGACAAACATGTGCCAGACAGTGGAGCCACAGCCACGG

E--> 245 CCTACCTGTGCGGGGTCAAGGGCAACTTCCAGACCATTGGCTTGAGTGCAGCCGCCCGC

E--> 246 TTTAACCAGTGCACACGACACGCGGCAACGAGGTCATCTCCGTGATGAATCGGGCCAA

E--> 247 GAAAGCAGGGAAGTCAGTGGGAGTGGTAACCACCACACGAGTGCAGCACGCCCTGCCAG

E--> 248 CCGGCACCTACGCCACACGGTGAACCGCAACTGGTACTCGGACGCCGACGTGCCTGCC

E--> 249 TCGGCCCGCCAGGAGGGGTGCCAGGACATCGCTACGCAGCTCATCTCCAACATGGACAT

E--> 250 TGACGTGATCCTAGGTGGAGGCCGAAAGTACATGTTTCCCATGGGAACCCCGAGCCCTG

E--> 251 AGTACCCAGATGACTACAGCCAAGGTGGGACCAGGCTGGACGGGAAGAATCTGGTGCA

E--> 252 GAATGGCTGGCGAAGCGCCAGGGTGCCCGGTATGTGTGGAACCGCACTGAGCTCATGCA

E--> 253 GGCTTCCCTGGACCCGTCTGTGACCCATCTCATGGGTCTCTTTGAGCCTGGAGACATGA

E--> 254 AATACGAGATCCACCGAGACTCCACACTGGACCCCTCCCTGATGGAGATGACAGAGGCT

E--> 255 GCCCTGCGCCTGCTGAGCAGGAACCCCGCGGCTTCTTCTCTTCGTGGAGGGTGGTCG

E--> 256 CATCGACCATGGTCATCATGAAAGCAGGGCTTACCGGGCACTGACTGAGACGATCATGT

E--> 257 TCGACGACGCCATGAGAGGGCGGGCCAGCTCACCAGCGAGGAGGACACGCTGAGCCCTC

E--> 258 GTCATGCGCAGCCACTCCCACTCTTCTTCTTCTCGGAGGCTACCCCTGCGAGGGAGCTC

E--> 259 CATCTTCGGGCTGGCCCTGGCAAGCGCCGGGACAGGAAGGCCTACACGGTCCCTCTAT

E--> 260 ACGGAAACGGTCCAGGCTATGTGCTCAAGGACGGCGCCCGCGGATGTTACCGAGAGC

E--> 261 GAGAGCGGGAGCCCCGAGTATCGGCAGCAGTCAGCAGTGGCCCTGGACGAAGAGACCCA

E--> 262 CGCAGGCGAGGACGTGGCGGTGTTTCGCGCGCGGCCCGCAGGCGCACCTGGTTACGGCG

Insert totals at end.

same errors

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E--> 263 TGCAGGAGCAGACCTTCATAGCGCACGTATGGCCTTCGCCGCCCTGCCTGGAGCCCTAC
 E--> 264 ACCGCCTGCGACCTGGCGCCCCCGCCGGCACCACCGACGCCGCGCACC CGGGTCCGG
 E--> 265 AGATCTGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCACCCTCAAGAG
 E--> 266 CCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGAAGCCGCAAGAACCCCGCCC
 E--> 267 GCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATT
 E--> 268 GACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGG
 E--> 269 TGAGACCTGCGTGTACCCCACTCAGCCCACTGTGGCCCAAGAAGTGGTACATCAGCA
 E--> 270 AGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAG
 E--> 271 TTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATGTGGCCATCCAGCTGACCTTCCT
 E--> 272 GCGCCTGATGTCCACCGAGGCCTCCGAGAACATCACCTACCCTGCAAGAACAGCGTGG
 E--> 273 CCTACATGGACACGAGACTGGCAACCTCAAGAAGGCCCTGCTCCTCAAGGGCTCCAAC
 E--> 274 GAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTACCTACAGCGTCACTGTGATGG
 E--> 275 CTGCACGAGTCACACCGGAGCCTGGGGCAAGACAGTGATTGAATACAAAACCACCAAGT
 E--> 276 CCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGTGCCCCAGACCAGGAA
 E--> 277 TTCGGCTTCGACCTTGGCCCTGTCTGCTTCTCTGTAACCTCCCTCCATCTAGA

Xba I

delete

Input
to also
end.

same
errors

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 755 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8

1	MLLLLLLLGL RLQSLGIIP VEEENPDFWN REAAEALGAA KKLQPAQTAA KNLIIFLGDG	60
61	MGVSTVTAAR ILKGQKDKL GPEIPLAMDR FPYVALSKTY NVDKHVPDSG ATATAYLCGV	120
121	KGNFQTIGLS AAARFNQCNT TRGNEVISVM NRAKKAGKSV GVVTTTRVQH ASPAGTYAHT	180
181	VNRNWYSDAD VPASARQEGC QDIATQLISN MDIDVILGGG RKYMFPMGTP DPEYPDDYSQ	240
241	GGTRLDGKNL VQEWLAKRQG ARYVWNRTLE MQASLDPSVT HLMGLFEPGD MKYEIHRDST	300
301	LDPSLMEMTE AALRLLSRNP RGFFLFVEGG RIDHGHESR AYRALTETIM FDDAIERAGQ	360
361	LTSEEDTSL VTADHSHVFS FGGYPLRGSS IFGLAPGKAR DRKAYTVLLY GNGPGYVLKD	420
421	GARPDVTESE SGSPEYRQOS AVPLDEETHA GEDVAVFARG PQAHLVHGVO EQTFIAHVMA	480
481	FAACLEPYTA CDLAPPAGTT DAAHPGSGRS DANVVRDRDL EVDTTLKSLQ QQIENIRSPE	540
541	GSRKNPARTC RDLKMCHSDW KSGEYWIDPN QGCNLDAIKV FCNMETGETC VYPTQPSVAQ	600
601	KNWYISKNP DKRHVWFGES MTDGFQFEYG GQGSDDADVA IQLTFLRLMS TEASQNITYH	660
661	CKNSVAYMDQ QTGNLKKALL LKGSNEIEIR AEGNSRFTYS VTVDGCTSHS GAWGKTIVIEY	720

same
errors

delete
#5

E--> 304 721 KTTKSSRLPI IDVAPLDVGA PDQEFQFDVG PVCFL
 307 (2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1734 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

W--> 314

W--> 315

316

317

RAW SEQUENCE LISTING

DATE: 04/09/2004

PATENT APPLICATION: US/10/677,877

TIME: 15:37:16

Input Set : A:\PTO.LN.txt

Output Set: N:\CRF4\04092004\J677877.raw

319 (vii) IMMEDIATE SOURCE:
 320 (B) CLONE: pTrimer/sTNFR1I-T0
 321 (ix) FEATURE:
 322 (A) NAME/KEY: CDS
 323 (B) LOCATION: 18..1718
 324 (D) OTHER INFORMATION:
 325 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9

E--> 327 ~~Bam HI~~ - delete
 E--> 328 GGATCCCGCCCGCACCCATGGCGCCCGTCGCCGCTCGGGCCGCGCTGGCCGTCGGACTGGAGCT
 E--> 329 CTGGGCTGCGGCGCACGCCCTTGCCCGCCAGGTGGCATTACACCCCTACGCCCCGAGCCCCGGG
 E--> 330 AGCACATGCCGGCTCAGAGAATACTATGACCAGACAGCTCAGATGTGCTGCAGCAAATGCTCGC
 E--> 331 CGGGCCAACATGAAAAGTCTTCTGTACCAAGACCTCGGACACCGTGTGTGACTCCTGTGAGGA
 E--> 332 CAGCACATACCCAGCTCTGGAAGTGGGTTCGAGTGTGAGCTGTGGCTCCCGCTGTAGC
 E--> 333 TCTGACCAGGTGGAAGTCAAGCCTGCACTCGGGAACAGAACCGCATCTGCACCTGCAGGCCCG
 E--> 334 GCTGGTACTGCGCGCTGAGCAAGCAGGAGGGGTGCCGGCTGTGCGCGCCGCTGCGCAAGTGCCG
 E--> 335 CCGGGGCTTCGGCGTGGCCAGACCAGGAAGTGAACATCAGACGTGGTGTGCAAGCCCTGTGCC
 E--> 336 CCGGGGACGTTCTCCAACACGACTTCATCCACGGATATTTGCAGGCCCCACCAGATCTGTAACG
 E--> 337 TGGTGGCCATCCCTGGGAATGCAAGCATGGATGCAGTCTGCACGTCCACGTCCCCACCCGGAG
 E--> 338 TATGGCCCCAGGGGAGTACACTTACCCAGCCAGTGTCCACACGATCCCAACACACGCAGCCA
 E--> 339 ACTCCAGAACCAGCACTGCTCCAAGCACCTCCTTCTGCTCCCAATGGGCCCCAGCCCCCAG
 E--> 340 CTGAAGGGAGCACTGGATCTAACGGTCTCCCTGGCCCCATTTGGGCCCCCTGGTCTCTCGCG
 E--> 341 TCGCACTGGTGATGCTGGTCTCTGTTGGTCCCCCGGCCCTCCTGGACCTCCTGGTCCCC
 E--> 342 CTGGTCTCTCCAGCGCTGGTTTCGACTTCAGCTTCCTGCCCCAGCCACCTCAAGAGAAG
 E--> 343 GCTCAGATGGTGGCCGCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGA
 E--> 344 CCTCGAGGTGGACACCACTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCC
 E--> 345 CAGAGGGAAGCCGCAAGAACCCTCGCCGACCTGCCGTGACCTCAAGATGTGCCACTCT
 E--> 346 GACTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCAT
 E--> 347 CAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAAGTG
 E--> 348 TGGCCCAAGAAGTGGTACATCAGCAAGAACCCTCAAGGACAAGAGGCATGTCTGGTTC
 E--> 349 GGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCCTGC
 E--> 350 CGATGTGGCCATCCAGCTGACCTTCCTGCGCCTGATGTCCACCGAGGCCCTCCAGAACA
 E--> 351 TCACCTACCACTGCAAGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAACCTCAAG
 E--> 352 AAGGCCCTGCTCCTCAAGGGCTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCG
 E--> 353 CTTACCTACAGCGTCACTGTGATGGCTGCACGAGTCACACCGGAGCCTGGGGCAAGA
 E--> 354 CAGTGATTGAATACAAAACCACCAAGTCTCCCGCCTGCCCATCATCGATGTGGCCCCC
 E--> 355 TTGGACGTTGGTGCCCCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCT
 E--> 356 GTAAACTCCCTCCATCTAGA
 E--> 357 ~~Xba I~~ - delete

Insert
to tail at
end.

same
errors

360 (2) INFORMATION FOR SEQ ID NO: 10:

361 (i) SEQUENCE CHARACTERISTICS:

362 (A) LENGTH: 566 amino acids

363 (B) TYPE: amino acid

364 (D) TOPOLOGY: linear

365 (ii) MOLECULE TYPE: protein

366 (vi) ORIGINAL SOURCE:

367 (A) ORGANISM: Homo sapiens

368 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10

371 1 MAPVAVWAAL AVGLELWAAA HALPAQVAFY PYAPEPGSTC RLREYYDQTA QMCCSKCSPG

372 61 QHAKVFCTKT SDTVCDSCED STYTQLWNWV PECLSCGSRC SSDQVETQAC TREQNRICTC

same
errors

delete
#s

delete
#s

RAW SEQUENCE LISTING

DATE: 04/09/2004

PATENT APPLICATION: US/10/677,877

TIME: 15:37:16

Input Set : A:\PTO.LN.txt

Output Set: N:\CRF4\04092004\J677877.raw

373 121 RPGWYCALSK QEGCRLCAPL RKCRPGFGVA RPGTETSDV CKPCAPGTFS NTTSSDICT 180
 374 181 PHQICNVVAI PGNASMDAVC TSTSPTRMA PGAVHLPQPV STRSQHTQPT PEPSTAPSTS 240
 375 241 FLLPMGPSPP AEGSTGSNGL PGPIGPPGPR GRTGDAGPVG PPGPPGPPGP PGPPSAGFDF 300
 376 301 SFLPQPPQEK AHDGGRIYRA DDANVVRDRD LEVDTTLSL SQIENIRSP EGSRKNPART 360
 377 361 CRDLKMHSD WKSGEYWIDP NQGCNLDAIK VFCNMETGET CVYPTQPSVA QKNWYISKNP 420
 378 421 KDKRHVWFGE SMTDGFQFEY GGQSDPADV AIQLTFLRLM STEASQNTY HCKNSVAYMD 480
 379 481 QQTGNLKKAL LLKGSNEIEI RAEGNSRFTY SVTVDGCTSH TGAWGKTIVIE YKTTKSSRLP 540

E--> 380 541 IIDVAPLDVG APDQEFGEFV GPVCFI

383 (2) INFORMATION FOR SEQ ID NO: 11:

384 (i) SEQUENCE CHARACTERISTICS:

385 (A) LENGTH: 1542 base pairs

386 (B) TYPE: nucleic acid

387 (C) STRANDEDNESS: double

388 (D) TOPOLOGY: linear

389 (ii) MOLECULE TYPE: cDNA

W--> 390 (iii) HYPOTHETICAL: N

W--> 391 (iv) ANTI-SENSE: N

392 (vi) ORIGINAL SOURCE:

393 (A) ORGANISM: Homo sapiens

395 (vii) IMMEDIATE SOURCE:

396 (B) CLONE: pTrimer/sTNFR1I-T2

397 (ix) FEATURE:

398 (A) NAME/KEY: CDS

399 (B) LOCATION: 18..1526

400 (D) OTHER INFORMATION:

401 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11

E--> 404 Bam HI
 E--> 405 GATCCCGCCCGCACCCATGGCGCCCGTCCGCGCTCTGGGCGCCGCTGGCCGCTCGGACTGGAGCT
 E--> 406 CTGGGCTGCGGCGCACGCCCTTGGCCGCCAGGTGGCATTTACACCCCTACGCCCGGAGCCCGGG
 E--> 407 AGCACATGCCGGCTCAGAGAATACTATGACCAGACAGCTCAGATGTGCTGCAGCAAATGCTCGC
 E--> 408 CGGGCCAACATGCAAAAGTCTTCTGTACCAAGACCTCGGACACCGTGTGTGACTCCTGTGAGGA
 E--> 409 CAGCACATACACCCAGCTCTGGAACCTGGGTTCCTGAGTGTGAGCTGTGGCTCCCGCTGTAGC
 E--> 410 TCTGACCAGGTGGAACCTCAAGCCTGCACTCGGGAACAGAACCGCATCTGCACCTGCAGGCCCG
 E--> 411 GCTGGTACTGCGCGCTGAGCAAGCAGGAGGGGTGCCGGCTGTGCGCGCCGCTGCGCAAGTGGCG
 E--> 412 CCCGGGCTTCGGCGTGGCCAGACCAGGAACCTGAAACATCAGACGTGGTGTGCAAGCCCTGTGCC
 E--> 413 CCGGGGACGTTCTCCAACACGACTTCATCCACGGATATTTGCAGGCCCCACCAGATCTGTAACG
 E--> 414 TGGTGGCCATCCCTGGGAATGCAAGCATGGATGCAGTCTGCACGTCCACGTCCCCCAGCCGGAG
 E--> 415 TATGGCCCCAGGGGAGTACACTTACCCAGCCAGTGTCCACACGATCCCAACACACGCGACCA
 E--> 416 ACTCCAGAACCAGCACTGCTCCAAGCACCTCCTTCTGCTCCCAATGGGCCCCAGCCCCCAG
 E--> 417 CTGAAGGGAGCACTGGATCTGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACAC
 E--> 418 CACCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGAAGCCGCA
 E--> 419 AGAACCCCGCCCGACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGA
 E--> 420 GAGTACTGGATTGACCCCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAA
 E--> 421 CATGGAGACTGGTGTGAGACCTGCGGTGTACCCCACTCAGCCCAAGTGTGGCCCAAGAACT
 E--> 422 GGTACATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACC
 E--> 423 GATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCCTGCCGATGTGGCCATCCA
 E--> 424 GCTGACCTTCTGCGCCTGATGTCCACCGAGGGCTCCCAAGAACATCACCTACCACTGCA
 E--> 425 AGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGCCCTGCTCCTC
 E--> 426 AAGGGCTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTCACCTACAGCGT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/677,877

DATE: 04/09/2004

TIME: 15:37:16

Input Set : A:\PTO.LN.txt

Output Set: N:\CRF4\04092004\J677877.raw

E--> 427 CACTGTCGATGGCTGCACGAGTCACACCGGAGCCTGGGGCAAGACAGTGATTGAATACA
 E--> 428 AAACCACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGTGCC
 E--> 429 CCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTGTAAACTCCCTCCAT
 E--> 430 CTAGA
 E--> 431 Xba I *delete*

Insert totals
same errors

434 (2) INFORMATION FOR SEQ ID NO: 12:

435 (i) SEQUENCE CHARACTERISTICS:

436 (A) LENGTH: 502 amino acids

437 (B) TYPE: amino acid

438 (D) TOPOLOGY: linear

439 (ii) MOLECULE TYPE: protein

440 (vi) ORIGINAL SOURCE:

441 (A) ORGANISM: Homo sapiens

442 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12

445	1	MAPVAVWAAL	AVGLELWAAA	HALPAQVAF	TYAPEPGSTC	RLREYYDQTA	QMCCSKCSPG	60
446	61	QHAKVFCTKT	SDTVCDSCED	STYTQLWNWV	PECLSCGSR	SSDQVETQAC	TREQNRICTC	120
447	121	RPGWYCALSK	QEGCRLCAPL	RKCRPGFGVA	RPGTETSDV	CKPCAPGTF	NTTSSTDICR	180
448	181	PHQICNVVAI	PGNASMDAV	TSTSPTRSMA	PGAVHLPQPV	STRSQHTQPT	PEPSTAPSTS	240
449	241	FLLPMGPSP	AEGSTGSDAN	VVRDRDLEVD	TTLKSLSQI	ENIRSPEGS	KNPARTCRDL	300
450	301	KMCHSDWKS	EYWIDPNQGC	NLDAIKVFCN	METGETCVYP	TQPSVAQKNW	YISKNPDKDR	360
451	361	HVWFGESMTD	GFQFEYGGQ	SDPADVAIQL	TFLRLMSTEA	QNITYHCKN	SVAYMDQQTG	420
452	421	NLKKALLK	G SNEIEIRAEG	NSRETYSVTV	DGCTSHTGAW	GKTVIEWKTT	KSSRLPIIDV	480

same errors

delete

E--> 453 481 APLDVGAPDQ EFGFDVGPVC FL

456 (2) INFORMATION FOR SEQ ID NO: 13:

457 (i) SEQUENCE CHARACTERISTICS:

458 (A) LENGTH: 2139 base pairs

459 (B) TYPE: nucleic acid

460 (C) STRANDEDNESS: double

461 (D) TOPOLOGY: linear

462 (ii) MOLECULE TYPE: cDNA

W--> 463 (iii) HYPOTHETICAL: N

W--> 464 (iv) ANTI-SENSE: N

465 (vi) ORIGINAL SOURCE:

466 (A) ORGANISM: Homo sapiens

468 (vii) IMMEDIATE SOURCE:

469 (B) CLONE: pTrimer/sCD4-T0

470 (ix) FEATURE:

471 (A) NAME/KEY: CDS

472 (B) LOCATION: 24..2123

473 (D) OTHER INFORMATION:

474 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13

E--> 477 Hind III *delete*
 E--> 478 AAGCTTCCCTCGGCCAAGGCCACAATGAACCGGGAGTCCCTTTTAGGCACCTGCTTCTG
 E--> 479 GTGCTGCAACTGGCGCTCCTCCCAGCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAA
 E--> 480 AAAAGGGGATACAGTGGAACTGACCTGTACAGCTTCCCAGAAGAAGAGCATACAATTCC
 E--> 481 ACTGGAAAACTCCAACCAGATAAAGATTCTGGGAAATCAGGGCTCCTTCTTAATAAA
 E--> 482 GGTCCATCCAAGCTGAATGATCGCGCTGACTCAAGAAGAAGCCTTTGGGACCAAGGAAA
 E--> 483 CTTTCCCCTGATCATCAAGAATCTTAAGATAGAAGACTCAGATACTTACATCTGTGAAG
 E--> 484 TGGAGGACCAGAAGGAGGAGGTGCAATTGCTAGTGTTCGGATTGACTGCCAACTCTGAC

Insert totals at end.

same errors

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/677,877

DATE: 04/09/2004

TIME: 15:37:16

Input Set : A:\PTO.LN.txt

Output Set: N:\CRF4\04092004\J677877.raw

E--> 485 ACCCACCTGCCTTCAGGGGCAGAGCCTGACCCTGACCTTGGAGAGCCCCCTGGTAGTAG
 E--> 486 CCCCTCAGTGCAATGTAGGAGTCCAAGGGGTAAAAACATACAGGGGGGGAAGACCCCTCT
 E--> 487 CCGTGTCTCAGCTGGAGCTCCAGGATAGTGGCACCTGGACATGCACCTGTCTTGCAGAAC
 E--> 488 CAGAAGAAGGTGGAGTTCAAAATAGACATCGTGGTGCTAGCTTTCCAGAAGGCCTCCAG
 E--> 489 CATAGTCTATAAGAAAGAGGGGGAACAGGTGGAGTTCTCCTTCCCACTCGCCTTTACAG
 E--> 490 TTGAAAAGCTGACGGGCAGTGGCGAGCTGTGGTGGCAGGCGGAGAGGGCTTCCTCCTCC
 E--> 491 AAGTCTTGGATCACCTTTGACCTGAAGAACAAGGAAGTGTCTGTAAACGGGTTACCCA
 E--> 492 GGACCCCTAAGCTCCAGATGGGCAAGAAGCTCCCGCTCCACCTCACCCTGCCCCAGGCCT
 E--> 493 TGCCTCAGTATGCTGGCTCTGGAACCTCACCCTGGCCCTTGAAGCGAAAAACAGGAAAG
 E--> 494 TTGCATCAGGAAGTGAACCTGGTGGTGATGAGAGCCACTCAGCTCCAGAAAAATTTGAC
 E--> 495 CTGTGAGGTGTGGGGACCCACCTCCCTTAAGCTGATGCTGAGCTTGAACCTGGAGAACA
 E--> 496 AGGAGGCAAAGGTCTCGAAGCGGGAGAAGGCGGTGTGGGTGCTGAACCCCTGAGGCGGGG
 E--> 497 ATGTGGCAGTGTCTGCTGAGTGACTCGGGACAGGTCTGCTGGAATCCAACATCAAGGT
 E--> 498 TCTGCCCAGATCTAACGGTCTCCCTGGCCCCATTGGGCCCCCTGGTCTCGCGGTGCGA
 E--> 499 CTGGTGATGCTGGTCTGTGGTCCCCCGGCCCTCCTGGACCTCCTGGTCCCCCTGGT
 E--> 500 CCTCCCAGCGCTGGTTTCGACTTCAGCTTCCTGCCCCAGCCACCTCAAGAGAAGGCTCA
 E--> 501 CGATGGTGGCCGCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCTCG
 E--> 502 AGGTGGACACCACCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAG
 E--> 503 GGAAGCCGCAAGAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTG
 E--> 504 GAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAG
 E--> 505 TCTTCTGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCC
 E--> 506 CAGAAGAACTGGTACATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGA
 E--> 507 GAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATG
 E--> 508 TGGCCATCCAGCTGACCTTCCTGCGCCTGATGTCCACCGAGGCCCTCCAGAACATCACC
 E--> 509 TACCCTGCAAGAACAGCGCTGGCCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGC
 E--> 510 CCTGCTCCTCAAGGGCTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTCA
 E--> 511 CCTACAGCGTCACTGTGATGGTGCACGAGTCAACCCGAGCCTGGGGCAAGACAGTG
 E--> 512 ATTGAATACAAAACCACCAAGTCCCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGG
 E--> 513 CGTTGGTGCCCCAGACCAGGAATTGGGCTTCGACGTTGGCCCTGTCTGCTTCTGTAA
 E--> 514 CTCCCTCCATCTAGA
 E--> 515

Xba I

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 699 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14

529	1	MNRGVPPFRL	LLVLQALLP	AATQGGKVV	L	GKGD	TVELT	CTASQKKS	IQ	FHWKNS	NQIK	60	
530	61	ILGNQGS	F	L	T	KGPSK	LNDR	DSRRSL	WDQ	G	NFPLI	KNL	120
531	121	LVFGLT	ANS	D	THLLQ	GQSL	T	LTLES	P	PGSS	PSVQ	CRSP	180
532	181	TWTCT	VLQ	NQ	KKVE	FKID	IV	VLAFQ	K	ASSI	VYK	EGEQ	240
533	241	QAERAS	SSKS	WIT	FDL	KNKE	VSVK	RVT	QDP	KLQ	MGK	KLPL	300
534	301	LEAKT	GKL	HQ	EVNL	V	MRAT	QLQ	KNL	TCE	V	WGPT	360
535	361	LNPEA	GMW	QC	LLSD	S	GQV	LL	ESNI	KV	LPRS	NGLP	420
536	421	PGPPG	PPS	AG	FDFS	FLP	QPP	QEK	AH	D	GGRY	YRADD	480
537	481	RSPEG	SRKN	P	ARTCR	DL	KMC	HSD	WKS	G	EYW	IDPN	540
												QGCNLD	
												AIKV	
												FCN	
												MET	
												GETC	
												VYPT	
												QTP	

Insert totals at the end.

same errors

same errors

delete

RAW SEQUENCE LISTING

DATE: 04/09/2004

PATENT APPLICATION: US/10/677,877

TIME: 15:37:16

Input Set : A:\PTO.LN.txt

Output Set: N:\CRF4\04092004\J677877.raw

538. 541 SVAQKNWYIS KNPDKRHHV FGESMTDGFQ FEYGGQGS DP ADVAIQLTFL RLMSTEASQN 600
 539 601 ITYHCKNSVA YMDQOTGNLK KALLKGSNE IEIRAEGNSR FTYSVTVDGC TSHTGAWGKT 660
 E--> 540 661 VIEYKTTKSS RLPIIDVAPL DVGAPDQEF G FDVGPVCFL
 544 (2) INFORMATION FOR SEQ ID NO: 15:
 545 (i) SEQUENCE CHARACTERISTICS:
 546 (A) LENGTH: 1947 base pairs
 547 (B) TYPE: nucleic acid
 548 (C) STRANDEDNESS: double
 549 (D) TOPOLOGY: linear
 550 (ii) MOLECULE TYPE: cDNA
 W--> 551 (iii) HYPOTHETICAL: N
 W--> 552 (iv) ANTI-SENSE: N
 553 (vi) ORIGINAL SOURCE:
 554 (A) ORGANISM: Homo sapiens
 556 (vii) IMMEDIATE SOURCE:
 557 (B) CLONE: pTrimer/sCD4-T2
 558 (ix) FEATURE:
 559 (A) NAME/KEY: CDS
 560 (B) LOCATION: 24..1931
 561 (D) OTHER INFORMATION:
 562 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15
 E--> 565 Hind III delete
 E--> 566 AAGCTTCCCTCGGCAAGGCCACAATGAACCGGGAGTCCCTTTAGGCACTTGCTTCTG
 E--> 567 GTGCTGCAACTGGCGCTCCTCCCAGCAGCCACTCAGGGAAGAAAGTGGTGTCTGGGCAA
 E--> 568 AAAAGGGGATACAGTGAACCTGACCTGTACAGCTTCCAGAAGAAGAGCATACAATTCC
 E--> 569 AACTGGAAAACTCCAACCATGAAAGATTCTGGGAAATCAGGGCTCCTTCTTAATAAA
 E--> 570 GGTCCATCCAAGCTGAATGATCGCGCTGACTCAAGAAGAAGCCCTTTGGGACCAAGGAAA
 E--> 571 CTTTCCCCTGATCATCAAGAATCTTAAGATAGAAGACTCAGATACTTACATCTGTGAAG
 E--> 572 TGGAGGACCAGAAGGAGGAGGTGCAATTGCTAGTGTTCGGATTGACTGCCAACTCTGAC
 E--> 573 ACCCACCTGCTTCAGGGGCAGAGCCTGACCTGACCTTGGAGAGCCCCCTGGTAGTAG
 E--> 574 CCCCTCAGTGCAATGTAGGAGTCCAAGGGGTAAAAACATACAGGGGGGAAGACCCCTCT
 E--> 575 CCGTGTCTCAGCTGGAGCTCCAGGATAGTGGCACCTGGACATGCACTGTCTTGAGAAC
 E--> 576 CAGAAGAAGGTGGAGTTCAAAATAGACATCGTGGTGTAGCTTCCAGAAGGCCTCCAG
 E--> 577 CATAGTCTATAAGAAAGAGGGGGAACAGGTGGAGTTCTCCTTCCCACTCGCCTTTACAG
 E--> 578 TTGAAAAGCTGACGGGCAGTGGCGAGCTGTGGTGGCAGGCGAGAGGGCTTCTCTCTCC
 E--> 579 AAGTCTTGGATCACCTTTGACCTGAAGAACAAGGAAGTGTCTGTAAAACGGGTTACCCA
 E--> 580 GGACCCTAAGCTCCAGATGGGCAAGAAGCTCCCGCTCCACCTCACCCTGCCCCAGGCCT
 E--> 581 TGCCTCAGTATGCTGGCTCTGGAAACCTCACCCTGGCCCTTGAAGCGAAAACAGGAAAG
 E--> 582 TTGCATCAGGAAGTGAACCTGGTGGTGTGATGAGAGCCACTCAGCTCCAGAAAAATTTGAC
 E--> 583 CTGTGAGGTGTGGGACCCACCTCCCCTAAGCTGATGCTGAGCTTGAAACTGGAGAACA
 E--> 584 AGGAGGCAAAGGTCTCGAAGCGGGAGAAGGCGGTGTGGGTGCTGAACCCCTGAGGCGGGG
 E--> 585 ATGTGGCAGTGTCTGCTGAGTGACTCGGGACAGGTCTGCTGGAATCCAACATCAAGGT
 E--> 586 TCTGCCAGATCTGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCACCC
 E--> 587 TCAAGAGCCTGAGCCAGCATCGAGAACATCCGGAGCCCAGAGGGAAGCCGCAAGAAC
 E--> 588 CCGCCCGCACCTGACCGGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTA
 E--> 589 CTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGG
 E--> 590 AGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCAAGAAGTGGTAC
 E--> 591 ATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGG
 E--> 592 ATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATGTGGCCATCCAGCTGA

RAW SEQUENCE LISTING

DATE: 04/09/2004

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Input Set : A:\PTO.LN.txt

Output Set: N:\CRF4\04092004\J677877.raw

E--> 593 CCTTCCTGCGCCTGATGTCCACCGAGGCCCTCCAGAACATCACCTACCACCTGCAAGAAC
 E--> 594 AGCGTGGCCCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGCCCTGCTCCTCAAGGG
 E--> 595 CTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTACCTACAGCGTCACTG
 E--> 596 TCGATGGCTGCACGAGTCACACCGGAGCCTGGGGCAAGACAGTGATTGAATACAAAACC
 E--> 597 ACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGTGCCCCAGA
 E--> 598 CCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTGTAAACTCCCTCCATCTAGA
 E--> 599

Xba I

delete

602 (2) INFORMATION FOR SEQ ID NO: 16:

603 (i) SEQUENCE CHARACTERISTICS:

604 (A) LENGTH: 635 amino acids

605 (B) TYPE: amino acid

606 (D) TOPOLOGY: linear

607 (ii) MOLECULE TYPE: protein

608 (vi) ORIGINAL SOURCE:

609 (A) ORGANISM: Homo sapiens

610 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16

613	1	MNRGVFPRHL	LLVLQLALLP	AATQGKRVVL	GKKGDTVELT	CTASQKKSIO	FHWKNSNQIK	60
614	61	ILGNQGSFLT	KGPSKLNDRA	DSRRSLWDQG	NFPLIKNLK	IEDSDTYICE	VEDQKEEVQL	120
615	121	LVFGLTANS	THLLQGQSLT	LTLESPPGSS	PSVQCRSPRG	KNIQGGKTLS	VSQLELQDSG	180
616	181	TWTCTVLQ	NQKKVEFKIDIV	VLAFAQASSI	VYKKEGEQVE	FSFPLAFTVE	KLTGSGELWW	240
617	241	QAERASSSKS	WITFDLKNKE	VSVKRVTDQP	KLQMGKKLPL	HLTLPQALPQ	YAGSGNLTLA	300
618	301	LEAKTGK	LHQEVNLVVMRAT	QLQKNLTCEV	WGPTSPKLML	SLKLENKEAK	VSKREKAVWV	360
619	361	LNPEAGM	WQCLLSDSGQVLL	ESNIKVLPRS	DANVVRDRDL	EVDTTLSLS	QQIENIRSPE	420
620	421	GSRKNPAR	TCRDLKMCHSDW	KSGEYWDPN	QGCNLDAIKV	FCNMETGETC	VYPTQPSVAQ	480
621	481	KNWYISK	NPKDKRHVWFES	MTDGFQFEYG	GQGSDDADVA	IQLTFLRLMS	TEASQNITYH	540
622	541	CKNSVAYM	DOQTGNLKKALL	LKGSNEIEIR	AEGNSRFTYS	VTVDGCTSH	GAWGKTVIEW	600
E--> 623	601	KTTKSSRL	PIIDVAPLDVGA	PDQEFQFDVG	PVCFL			

* FYI: All U.S. applications filed on or after July 1, 1998, and which cannot claim a prior application filed before July 1, 1998, must use the "new" Sequence Rules format. This sequence listing is in "old" Sequence Rules format.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/677,877

DATE: 04/09/2004

TIME: 15:37:17

Input Set : A:\PTO.LN.txt

Output Set: N:\CRF4\04092004\J677877.raw

L:0 M:200 E: Mandatory Header Field missing, [(i) APPLICANT:] of (1)
 L:0 M:200 E: Mandatory Header Field missing, [(ii) TITLE OF INVENTION:] of (1)
 L:0 M:200 E: Mandatory Header Field missing, [(A) ADDRESSEE:] of (1)(iv)
 L:0 M:200 E: Mandatory Header Field missing, [(B) STREET:] of (1)(iv)
 L:0 M:200 E: Mandatory Header Field missing, [(C) CITY:] of (1)(iv)
 L:0 M:200 E: Mandatory Header Field missing, [(D) STATE:] of (1)(iv)
 L:0 M:200 E: Mandatory Header Field missing, [(E) COUNTRY:] of (1)(iv)
 L:0 M:200 E: Mandatory Header Field missing, [(F) ZIP:] of (1)(iv)
 L:0 M:249 C: Inserted Mandatory Field, [(vi) CURRENT APPLICATION DATA:]
 L:0 M:249 C: Inserted Mandatory Field, [(A) APPLICATION NUMBER:]
 L:0 M:249 C: Inserted Mandatory Field, [(B) FILING DATE:]
 L:13 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=1
 L:14 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=1
 L:27 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
 L:27 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:28 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:28 M:254 E: No. of Bases conflict, Input:0 Counted:55 SEQ:1
 M:254 Repeated in SeqNo=1
 L:46 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:46 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:64 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:64 M:330 E: (2) Invalid Amino Acid Designator, 2
 L:64 M:203 E: No. of Seq. differs, LENGTH:Input:311 Found:2 SEQ:2
 L:74 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=3
 L:75 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=3
 L:88 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
 L:88 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:89 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:89 M:254 E: No. of Bases conflict, Input:0 Counted:64 SEQ:3
 M:254 Repeated in SeqNo=3
 L:102 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:102 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:120 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:120 M:330 E: (2) Invalid Amino Acid Designator, 1
 L:120 M:203 E: No. of Seq. differs, LENGTH:Input:247 Found:1 SEQ:4
 L:130 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=5
 L:131 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=5
 L:144 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:144 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:145 M:254 E: No. of Bases conflict, Input:0 Counted:59 SEQ:5
 M:254 Repeated in SeqNo=5
 L:188 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:188 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:215 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:215 M:330 E: (2) Invalid Amino Acid Designator, 4
 L:215 M:203 E: No. of Seq. differs, LENGTH:Input:819 Found:4 SEQ:6
 L:225 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=7
 L:226 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=7

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/677,877

DATE: 04/09/2004

TIME: 15:37:17

Input Set : A:\PTO.LN.txt

Output Set: N:\CRF4\04092004\J677877.raw

L:238 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:238 M:333 E: Wrong sequence grouping, Amino acids not in groups! ✓
 L:239 M:254 E: No. of Bases conflict, Input:0 Counted:59 SEQ:7 ✓
 M:254 Repeated in SeqNo=7
 L:278 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:278 M:333 E: Wrong sequence grouping, Amino acids not in groups! ✓
 L:304 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:304 M:330 E: (2) Invalid Amino Acid Designator, 4 ✓
 L:304 M:203 E: No. of Seq. differs, LENGTH:Input:755 Found:4 SEQ:8 ✓
 L:314 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=9
 L:315 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=9
 L:327 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:327 M:333 E: Wrong sequence grouping, Amino acids not in groups! ✓
 L:328 M:254 E: No. of Bases conflict, Input:0 Counted:64 SEQ:9
 M:254 Repeated in SeqNo=9
 L:357 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:357 M:333 E: Wrong sequence grouping, Amino acids not in groups! ✓
 L:380 M:333 E: Wrong sequence grouping, Amino acids not in groups! ✓
 L:380 M:330 E: (2) Invalid Amino Acid Designator, 3 ✓
 L:380 M:203 E: No. of Seq. differs, LENGTH:Input:566 Found:3 SEQ:10 ✓
 L:390 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=11
 L:391 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=11
 L:404 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:404 M:333 E: Wrong sequence grouping, Amino acids not in groups! ✓
 L:405 M:254 E: No. of Bases conflict, Input:0 Counted:64 SEQ:11 ✓
 M:254 Repeated in SeqNo=11
 L:431 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:431 M:333 E: Wrong sequence grouping, Amino acids not in groups! ✓
 L:453 M:333 E: Wrong sequence grouping, Amino acids not in groups! ✓
 L:453 M:330 E: (2) Invalid Amino Acid Designator, 3 ✓
 L:453 M:203 E: No. of Seq. differs, LENGTH:Input:502 Found:3 SEQ:12 ✓
 L:463 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=13
 L:464 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=13
 L:477 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:477 M:333 E: Wrong sequence grouping, Amino acids not in groups! ✓
 L:478 M:254 E: No. of Bases conflict, Input:0 Counted:59 SEQ:13 ✓
 M:254 Repeated in SeqNo=13
 L:515 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:515 M:333 E: Wrong sequence grouping, Amino acids not in groups! ✓
 L:540 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:540 M:330 E: (2) Invalid Amino Acid Designator, 4 ✓
 L:540 M:203 E: No. of Seq. differs, LENGTH:Input:699 Found:4 SEQ:14 ✓
 L:551 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=15
 L:552 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=15
 L:565 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:565 M:333 E: Wrong sequence grouping, Amino acids not in groups! ✓
 L:566 M:254 E: No. of Bases conflict, Input:0 Counted:59 SEQ:15 ✓
 M:254 Repeated in SeqNo=15
 L:599 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2

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L:599 M:333 E: Wrong sequence grouping, Amino acids not in groups! ✓
 L:623 M:333 E: Wrong sequence grouping, Amino acids not in groups! ✓
 L:623 M:330 E: (2) Invalid Amino Acid Designator, 4 ✓
 L:623 M:203 E: No. of Seq. differs, LENGTH:Input:635 Found:4 SEQ:16 ✓